

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2005, 12:06:06 ; Search time 20.4938 Seconds
(without alignments)
1674.182 Million cell updates/sec

Title: US-09-609-146-4

Perfect score: 2185

Sequence: 1 MSGMEKLNQASWIIQKLED.....ALSSEQMSRTYQSFHNKT 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2185	100.0	415	2	US-09-875-076-12
2	2170	99.3	412	2	US-09-949-016-10101
3	2162	98.9	415	2	US-09-545-944-2
4	2162	98.9	415	2	US-10-215-619-2
5	2148	98.3	415	2	US-09-341-016A-1
6	1252	57.3	242	2	US-09-684-725-2
7	942	43.1	403	2	US-09-170-496D-114
8	942	43.1	403	2	US-09-170-496D-224
9	942	43.1	403	2	US-09-743-742B-4
10	942	43.1	403	2	US-09-743-742B-10
11	825.5	37.8	405	2	US-09-743-742B-2
12	825.5	37.8	405	2	US-09-743-742B-11
13	476	21.8	412	2	US-09-743-742B-8
14	471	21.6	418	2	US-09-743-742B-5
15	471	21.6	418	2	US-09-826-509-535
16	448	20.5	353	2	US-09-077-675A-3
17	448	20.5	353	2	US-09-077-674-3
18	448	20.5	366	2	US-09-762-661A-7
19	448	20.5	366	2	US-09-743-475-6
20	447	20.5	366	2	US-09-170-496D-210
21	444	20.3	361	2	US-09-077-675A-8
22	444	20.3	361	2	US-09-077-674-8
23	444	20.3	366	2	US-09-077-675A-13
24	444	20.3	366	2	US-09-077-674-13
25	444	20.3	366	2	US-09-170-496D-88
26	444	20.3	366	2	US-09-743-742B-7
27	444	20.3	366	2	US-09-762-661A-5

28	444	20.3	366	2	US-09-364-425B-45	Sequence 45, Appl
29	444	20.3	366	2	US-09-743-475-4	Sequence 4, Appl
30	436.5	20.0	364	2	US-09-077-675A-16	Sequence 16, Appl
31	436.5	20.0	364	2	US-09-077-674-16	Sequence 16, Appl
32	436.5	20.0	364	2	US-09-762-661A-6	Sequence 6, Appl
33	436.5	20.0	364	2	US-09-743-475-5	Sequence 5, Appl
34	436.5	19.9	364	2	US-09-743-475-3	Sequence 3, Appl
35	430	19.7	349	2	US-09-762-661A-2	Sequence 2, Appl
36	417.5	19.1	353	1	US-08-118-270-45	Sequence 45, Appl
37	417.5	19.1	353	4	FCT-US93-08528-45	Sequence 45, Appl
38	410	18.8	415	2	US-09-743-742B-6	Sequence 6, Appl
39	410	18.8	416	2	US-08-858-876A-4	Sequence 4, Appl
40	410	18.8	416	2	US-09-472-880-4	Sequence 4, Appl
41	405.5	18.6	398	1	US-08-288-663A-1	Sequence 1, Appl
42	402	18.4	302	2	US-09-077-675A-2	Sequence 2, Appl
43	402	18.4	302	2	US-09-077-674-2	Sequence 2, Appl
44	398	18.2	302	2	US-09-077-675A-7	Sequence 7, Appl
45	398	18.2	302	2	US-09-077-674-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-875-076-12
; Sequence 12, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281

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OM protein - protein search, using sw model

Run on: November 19, 2005, 19:53:11 ; Search time 54.3086 Seconds
(without alignments)
3192.847 Million cell updates/sec

Title: US-09-609-146-4

Perfect score: 2185

Sequence: 1 MSGMEKLQNASWIYQOKLED.....ALSSQMSRTYQSPHNKT 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	100.0	415	3	US-09-875-076-12
2	2185	100.0	415	3	US-09-876-252-12
3	2185	100.0	415	4	US-10-272-983-12
4	2185	100.0	415	4	US-10-393-807-12
5	2185	100.0	415	4	US-10-258-423-2
6	2185	100.0	415	4	US-10-417-820A-12
7	2185	100.0	415	4	US-10-723-955-12
8	2185	100.0	415	4	US-10-782-596-12
9	2185	100.0	415	4	US-10-203-015A-1
10	2185	100.0	415	4	US-10-770-583-2
11	2185	100.0	415	5	US-10-723-955-12
12	2185	100.0	415	5	US-10-745-237-396
13	2170	99.3	412	4	US-10-225-567A-557
14	2170	99.3	412	4	US-10-770-583-4
15	2166	99.1	415	4	US-10-203-015A-17
16	2162	98.9	415	4	US-10-770-583-6
17	2162	98.9	415	5	US-10-215-619-2
18	2148	98.3	415	5	US-10-890-407A-1
19	2147	98.3	412	4	US-10-770-583-8
20	2113	96.7	402	4	US-10-258-423-4
21	1650.5	75.5	395	4	US-10-258-423-6
22	1643.5	75.5	396	4	US-10-258-423-8
23	1409	64.5	296	4	US-10-203-015A-21
24	1394	63.8	293	4	US-10-770-583-10
25	1252	57.3	242	5	US-10-915-157-2
26	1251	57.3	249	3	US-09-782-974C-18
27					

28	1251	57.3	249	5	US-10-467-492A-18	Sequence 18, Appl
29	1251	57.3	249	5	US-10-975-979-18	Sequence 18, Appl
30	1251	57.3	249	5	US-10-969-727-18	Sequence 18, Appl
31	942	43.1	403	4	US-10-251-385-114	Sequence 114, Appl
32	942	43.1	403	4	US-10-251-385-224	Sequence 224, Appl
33	942	43.1	403	4	US-10-225-567A-540	Sequence 540, Appl
34	942	43.1	403	4	US-10-290-078-18	Sequence 18, Appl
35	942	43.1	403	4	US-10-353-690-10	Sequence 10, Appl
36	942	43.1	403	5	US-10-915-157-8	Sequence 8, Appl
37	941	43.1	426	4	US-10-712-124-116	Sequence 116, Appl
38	939	43.0	445	4	US-10-240-145-53	Sequence 53, Appl
39	939	43.0	445	4	US-10-240-145-139	Sequence 139, Appl
40	939	43.0	445	5	US-10-291-128-53	Sequence 53, Appl
41	939	43.0	445	5	US-10-291-128-139	Sequence 139, Appl
42	929	42.5	426	4	US-10-311-671-1	Sequence 1, Appl
43	929	42.5	426	6	US-11-100-583-1	Sequence 1, Appl
44	921	42.2	422	4	US-10-367-094-141	Sequence 141, Appl
45	804.5	36.8	403	4	US-10-367-094-138	Sequence 138, Appl

ALIGNMENTS

RESULT 1
US-09-875-076-12
; Sequence 12, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
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; PRIOR APPLICATION NUMBER: 60/136,436
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; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281

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OM protein - protein search, using sw model

Run on: November 19, 2005, 20:08:37 ; Search time 4.61111 Seconds
(without alignments)
101.661 Million cell updates/sec

Title: US-09-609-146-4
Perfect score: 2185
Sequence: 1 MSGMEKLQNASWIYQKLED.....ALSSEQMSRTWYQSFHFKT 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
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8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	12.3	522	1	US-10-510-018-2
2	242.5	11.1	350	1	US-10-502-145-1
3	236.5	10.8	415	1	US-10-627-633-2
4	235	10.8	409	1	US-10-627-633-4
5	233	10.7	352	1	US-10-627-633-6
6	142.5	6.5	347	1	US-10-131-826A-18
7	85.5	3.9	446	7	US-11-082-389-316
8	81.5	3.7	693	1	US-10-131-826A-406
9	81	3.7	426	7	US-11-008-331-2
10	78.5	3.6	327	1	US-10-467-962B-107
11	77	3.5	472	7	US-11-008-331-3
12	75.5	3.5	765	1	US-10-131-826A-28
13	74	3.4	508	7	US-11-082-389-178
14	73	3.3	463	1	US-10-510-386-186
15	72.5	3.3	3056	7	US-11-109-156-20
16	70	3.2	628	7	US-11-082-389-402
17	69.5	3.2	263	7	US-11-082-389-120
18	69.5	3.2	278	7	US-11-082-389-118
19	69.5	3.2	453	7	US-11-082-389-198
20	69.5	3.2	926	1	US-10-841-129-2
21	69.5	3.2	928	1	US-10-841-129-6
22	68.5	3.1	464	1	US-10-689-742-164
23	68	3.1	435	1	US-10-510-386-62
24	68	3.1	928	1	US-10-841-129-4
25	67	3.1	348	7	US-11-082-389-218

26	67	3.1	582	7	US-11-074-176-110	Sequence 110, App
27	66	3.0	324	7	US-11-082-389-440	Sequence 440, App
28	66	3.0	480	7	US-11-074-176-2	Sequence 2, Appl
29	65.5	3.0	585	7	US-11-012-762-6	Sequence 6, Appl
30	65.5	3.0	1167	1	US-10-942-072-6	Sequence 6, Appl
31	65	3.0	394	7	US-11-074-176-310	Sequence 310, App
32	65	3.0	414	7	US-11-074-176-46	Sequence 46, Appl
33	65	3.0	643	7	US-11-074-176-318	Sequence 318, App
34	65	3.0	667	7	US-11-074-176-64	Sequence 64, Appl
35	64.5	3.0	135	7	US-11-082-389-414	Sequence 414, App
36	64.5	3.0	604	1	US-10-942-072-4	Sequence 4, Appl
37	64.5	3.0	1167	1	US-10-942-072-13	Sequence 13, Appl
38	64.5	3.0	1168	1	US-10-942-072-11	Sequence 11, Appl
39	64	2.9	849	1	US-10-467-962B-53	Sequence 53, Appl
40	63.5	2.9	391	7	US-11-082-389-172	Sequence 172, App
41	63.5	2.9	391	7	US-11-082-389-174	Sequence 174, App
42	63.5	2.9	395	7	US-11-074-176-188	Sequence 188, App
43	63.5	2.9	690	1	US-10-131-826A-306	Sequence 306, App
44	63.5	2.9	1049	1	US-10-131-826A-358	Sequence 358, App
45	63.5	2.9	2897	1	US-10-499-715-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-510-018-2
; Sequence 2, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 2 (NPFF2)
; FILE REFERENCE: Le A 35 945
; CURRENT APPLICATION NUMBER: US/10/510,018
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/002962
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: EP 02007270.8
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-018-2

Query Match	12.3%	Score 268;	DB 1;	Length 522;
Best Local Similarity	22.3%	Pred. No. 6.4e-21;		
Matches	90;	Conservative	88;	Mismatches 168;
				Indels 58; Gaps 13;
QY	25	HLNSTEYL-----AFLCGRSRSHFFLPVSVVYVIFVVGVIIGNVLVCLVLOHQ	74	
DB	120	NVNDTRHLYSDINITYVNYLHPQVAAIFI---ISYFLIFELCMGNTVWCVFVVRNK	176	
QY	75	AMKTPNYLFSLVSDLLVLLGLGMPLEVE-MWRNYPELFGVGVCFKALFETVCFAS	133	
DB	177	HHHTVTNLFILNLSLDLLVGFPCMTILDNIAGWP--FGNTMKISGLVQGISVAAS	234	
QY	134	ILSITTVSVERVVAIIHPFRALQSTRRALRILGIVWGFSLVFLPNTSIHGKHYFP	193	
DB	235	VTLVAIVDRQCVCVYVPEPKL--TIKTAFLIIMLIWLIATIMFSVAMLVHQEKKY	292	
QY	194	NSGLVPGSATCTV--IKPMW-----IYNFIQVTSFLF---YLLPMTVISVLYLMAL	241	
DB	293	RVLANSQNTSPVYWCREDWPNQMKIV-----TTLFANIYLAFLSLIVIMYGRIGI	346	
QY	242	RLKKDKSLSEADSGNAN-----IOPCKSVNKMFLVILVLPACWAPHDRFLFFSVFEW	297	
DB	347	SLFRAAVPHTRGRKNOEQMHVSRKKQKII-KMLLVALLFILSLWPLTMTMLMSDYADLS	405	

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OM protein - protein search, using sw model

Run on: November 19, 2005, 20:08:37 ; Search time 4.38889 Seconds
(without alignments)
101.681 Million cell updates/sec

Title: US-09-609-146-25

Perfect score: 2076

Sequence: 1 MGKLENASWTHDPLMKYLS.....GQSHHTNLTTPACGVP 395.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301	14.5	522	1	US-10-510-018-2
2	252.5	12.2	409	1	US-10-627-633-4
3	251.5	12.1	415	1	US-10-627-633-2
4	247.5	11.9	352	1	US-10-627-633-6
5	227.5	11.0	350	1	US-10-502-145-1
6	147.5	7.1	347	1	US-10-131-826A-18
7	95.5	4.6	582	7	US-11-074-176-110
8	89	4.3	446	7	US-11-082-389-316
9	77	3.7	453	7	US-11-082-389-198
10	75	3.6	579	1	US-10-975-798-4
11	75	3.6	580	1	US-10-975-798-3
12	73.5	3.5	394	7	US-11-074-176-310
13	73.5	3.5	414	7	US-11-074-176-46
14	72.5	3.5	928	1	US-10-841-129-4
15	71	3.4	928	1	US-10-841-129-6
16	69.5	3.3	472	7	US-11-008-331-3
17	69.5	3.3	508	7	US-11-082-389-178
18	69	3.3	3056	7	US-11-109-156-20
19	68.5	3.3	765	1	US-10-131-826A-28
20	68.5	3.3	1049	1	US-10-131-826A-358
21	67	3.2	628	7	US-11-082-389-402
22	67	3.2	639	7	US-11-074-176-222
23	66.5	3.2	1167	1	US-10-942-072-6
24	66	3.2	693	1	US-10-131-826A-406
25	66	3.2	926	1	US-10-841-129-2

26	65.5	3.2	426	1	US-10-131-826A-218	Sequence 218, App
27	65	3.1	463	1	US-10-510-386-186	Sequence 186, App
28	64.5	3.1	426	7	US-11-008-331-2	Sequence 2, Appli
29	64.5	3.1	482	1	US-10-689-742-66	Sequence 66, Appl
30	64.5	3.1	1167	1	US-10-942-072-13	Sequence 13, Appl
31	64.5	3.1	1168	1	US-10-942-072-11	Sequence 11, Appl
32	63.5	3.1	373	7	US-11-082-389-200	Sequence 200, App
33	63	3.0	348	7	US-11-082-389-218	Sequence 218, App
34	63	3.0	395	7	US-11-074-176-188	Sequence 188, App
35	63	3.0	888	7	US-11-077-550-112	Sequence 112, App
36	62.5	3.0	456	7	US-11-074-176-238	Sequence 238, App
37	62	3.0	539	1	US-10-131-826A-140	Sequence 140, App
38	61.5	3.0	750	1	US-10-689-742-86	Sequence 86, Appl
39	61.5	3.0	817	7	US-11-012-762-2	Sequence 2, Appli
40	61	2.9	350	7	US-11-082-389-380	Sequence 380, App
41	60.5	2.9	1420	7	US-11-077-550-110	Sequence 110, App
42	59.5	2.9	316	7	US-11-082-389-62	Sequence 62, Appl
43	59	2.8	458	7	US-11-077-550-114	Sequence 114, App
44	59	2.8	548	7	US-11-077-550-24	Sequence 24, Appl
45	59	2.8	858	7	US-11-077-550-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-10-510-018-2
; Sequence 2, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 2 (NPFF2)
; FILE REFERENCE: Le A 35 945
; CURRENT APPLICATION NUMBER: US/10/510.018
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/BP2003/002962
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: EP 02007270.8
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-510-018-2

Query Match	14.5%	Score 301;	DB 1;	Length 522;
Best Local Similarity	23.8%	Pred. No. 3.9e-23;		
Matches	81;	Conservative	83;	Mismatches 151;
				Indels 26;
				Gaps 9;
Qy	42	VAVALIFGVGMGNLLVCMVIVRHQTKPTNYLPSLAVSDLLVLLGMPLEIYE-MWH	100	
Db	152	ISYFLFFLCMGNTVCCIVMKNKHEHTVNLFILNLAISDLLGVFCPIILLDIIA	211	
Qy	101	NYPLFGPVGCTKATLFTVCFASILSVTVSVRYVAIVHFPRAKLESTRRLRLILS	160	
Db	212	GMP--FGNTWCKISGLVQGISVAASVFTLVAIAVDRCVQVVPFKPL--TKTAPVIIM	267	
Qy	161	LWSPSVVPSLNTSHGKIFQHPNGSSVPGSATCTV--TKPMW-----VYNLIQA	211	
Db	268	ILWLATITMSAVMLHQEEKYVRNLNSQNTKSPVTWCREDWPNQEKRIYTTVLFA	327	
Qy	212	TSFLFYLPMTLISLVLYLMGLRLKE---DESLEANKVAIVNIHRPSKSVTKMLFVLV	268	
Db	328	N---LYLAPLSLIVIMYGRIGISLFRAAVPHTRGNQEQHWVSRKKQIKIMLLIVALL	384	
Qy	269	PAICWTPHVDRLFRFSFVEWETESLAAPNLIHVSGVFYLLSSAVNPITYNLLSRFPRA	328	
Db	385	FILSWLPLMTLMLSDYADLSNELQIINIYIYPPAHMLAFGNSSVNPITYGFFNFENFR	444	

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OM protein - protein search, using sw model

Run on: November 19, 2005, 19:53:11 ; Search time 51.6914 Seconds
(without alignments)
3192.847 Million cell updates/sec

Title: US-09-609-146-25

Perfect score: 2076

Sequence: 1 MGKLENASWIHDPLMKYLNS.....GOSSIHNTLTTAPCAGEVP 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2076	100.0	395	4	US-10-258-423-6
2	2076	100.0	396	4	US-10-258-423-8
3	2063	99.4	395	4	US-10-203-015A-21
4	1650.5	79.5	402	4	US-10-258-423-4
5	1650.5	79.5	412	4	US-10-225-567A-557
6	1650.5	79.5	412	4	US-10-770-583-4
7	1650.5	79.5	415	3	US-09-875-076-12
8	1650.5	79.5	415	3	US-09-876-252-12
9	1650.5	79.5	415	4	US-10-272-983-12
10	1650.5	79.5	415	4	US-10-393-807-12
11	1650.5	79.5	415	4	US-10-258-423-2
12	1650.5	79.5	415	4	US-10-417-820A-12
13	1650.5	79.5	415	4	US-10-723-955-12
14	1650.5	79.5	415	4	US-10-782-596-12
15	1650.5	79.5	415	4	US-10-203-015A-1
16	1650.5	79.5	415	4	US-10-770-583-2
17	1650.5	79.5	415	5	US-10-723-955-12
18	1650.5	79.5	415	5	US-10-745-237-396
19	1644.5	79.2	415	4	US-10-203-015A-17
20	1640.5	79.0	412	4	US-10-770-583-8
21	1640.5	79.0	415	4	US-10-770-583-6
22	1640.5	79.0	415	5	US-10-215-619-2
23	1632.5	78.6	415	5	US-10-890-407A-1
24	1117.5	53.8	293	4	US-10-770-583-12
25	1117.5	53.8	296	4	US-10-770-583-10
26	1035.5	49.8	242	5	US-10-915-157-2
27	1022.5	49.3	249	3	US-09-782-974C-18

28	1022.5	49.3	249	5	US-10-467-492A-18	Sequence 18, Appl
29	1022.5	49.3	249	5	US-10-975-979-18	Sequence 18, Appl
30	1022.5	49.3	249	5	US-10-969-727-18	Sequence 18, Appl
31	952.5	45.9	403	4	US-10-251-385-114	Sequence 114, App
32	952.5	45.9	403	4	US-10-225-567A-540	Sequence 540, App
33	952.5	45.9	403	4	US-10-290-078-18	Sequence 18, Appl
34	952.5	45.9	403	4	US-10-353-690-10	Sequence 10, Appl
35	952.5	45.9	403	5	US-10-915-157-8	Sequence 8, Appl
36	951.5	45.8	426	4	US-10-712-124-116	Sequence 116, App
37	949.5	45.7	445	4	US-10-240-145-53	Sequence 53, Appl
38	949.5	45.7	445	4	US-10-240-145-139	Sequence 139, App
39	949.5	45.7	445	5	US-10-291-128-53	Sequence 53, Appl
40	949.5	45.7	445	5	US-10-291-128-139	Sequence 139, App
41	946.5	45.6	403	4	US-10-251-385-224	Sequence 224, App
42	939.5	45.3	426	4	US-10-311-671-1	Sequence 1, Appl
43	939.5	45.3	426	6	US-11-100-583-1	Sequence 1, Appl
44	933	44.9	422	4	US-10-367-094-141	Sequence 141, App
45	819	39.5	403	4	US-10-367-094-138	Sequence 138, App

ALIGNMENTS

RESULT 1
US-10-258-423-6
; Sequence 6, Application US/10258423
; Publication No. US20030211968A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: University of Virginia
; TITLE OF INVENTION: NEW NEUROMEDIN U RECEPTOR NMUR2/AND
; FILE REFERENCE: NUCLEOTIDES ENCODING IT
; FILE REFERENCE: 20658P
; CURRENT APPLICATION NUMBER: US/10/258,423
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/200,718
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Rattus
US-10-258-423-6

Query Match		100.0%;	Score 2076;	DB 4;	Length 395;
Best Local Similarity		100.0%;	Pred. No. 4e-174;		
Matches		395;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MGKLENASWIHDPLMKYLNS	TEYLALHLCGPKGSDLSLPVS	VAYALFLVGMGNLLVCM	60
Db	1	MGKLENASWIHDPLMKYLNS	TEYLALHLCGPKGSDLSLPVS	VAYALFLVGMGNLLVCM	60
Qy	61	VIVRHQTLKTPNTNYL	FLSLAVSDLLVLLGMPLEI	YEMHNYPFLFGVGCYKTA	120
Db	61	VIVRHQTLKTPNTNYL	FLSLAVSDLLVLLGMPLEI	YEMHNYPFLFGVGCYKTA	120
Qy	121	VCFASTLSVTVSVRYVAI	VHPFRALRILSLVWSFVS	VPSPNTSIHGK	180
Db	121	VCFASTLSVTVSVRYVAI	VHPFRALRILSLVWSFVS	VPSPNTSIHGK	180
Qy	181	FOHPPNGSSVPGSATCT	VTKPMVYNNLIIOATSF	FLYILPMTLISVLVYLMGLR	240
Db	181	FOHPPNGSSVPGSATCT	VTKPMVYNNLIIOATSF	FLYILPMTLISVLVYLMGLR	240
Qy	241	LEANKVAVNIHRPSKSV	TNQLFVLVLPFAICWTP	PHVDRLPFSFVEEWTES	300
Db	241	LEANKVAVNIHRPSKSV	TNQLFVLVLPFAICWTP	PHVDRLPFSFVEEWTES	300
Qy	301	HVYSGVFFYLSSAVN	PIIYNLSRRFRAAFRN	VSTCKWCHRRHRRPQGP	360
Db	301	HVYSGVFFYLSSAVN	PIIYNLSRRFRAAFRN	VSTCKWCHRRHRRPQGP	360

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2005, 12:06:06 ; Search time 19.5062 Seconds
(without alignments)
1674.182 Million cell updates/sec

Title: US-09-609-146-25

Perfect score: 2076

Sequence: 1 MGKLENASWIHDFLMKYLNS.....GQSSIHTNLTTPACAGEVP 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1650.5	79.5	412	2	US-09-949-016-10101
2	1650.5	79.5	415	2	US-09-875-076-12
3	1640.5	79.0	415	2	US-09-545-944-2
4	1640.5	79.0	415	2	US-10-215-619-2
5	1632.5	78.6	415	2	US-09-341-016A-1
6	1033.5	49.8	242	2	US-09-684-725-2
7	952.5	45.9	403	2	US-09-170-496D-114
8	952.5	45.9	403	2	US-09-743-742B-4
9	952.5	45.9	403	2	US-09-743-742B-10
10	946.5	45.6	403	2	US-09-170-496D-224
11	840	40.5	405	2	US-09-743-742B-2
12	840	40.5	405	2	US-09-743-742B-11
13	499	24.0	418	2	US-09-743-742B-5
14	498	24.0	418	2	US-09-826-509-535
15	477.5	23.0	412	2	US-09-743-742B-8
16	465.5	22.4	364	2	US-09-743-742B-16
17	465.5	22.4	364	2	US-09-077-675A-16
18	465.5	22.4	364	2	US-09-077-674-16
19	465.5	22.4	364	2	US-09-762-661A-6
20	465	22.4	353	2	US-09-743-475-5
21	465	22.4	353	2	US-09-077-675A-3
22	465	22.4	364	2	US-09-077-674-3
23	465	22.4	366	2	US-09-743-475-3
24	465	22.4	366	2	US-09-762-661A-7
25	463.5	22.3	361	2	US-09-743-475-6
26	463.5	22.3	361	2	US-09-077-675A-8
27	463.5	22.3	366	2	US-09-077-674-8
					Sequence 13, Appl

28 463.5 22.3 366 2 US-09-077-674-13 Sequence 13, Appl
29 463.5 22.3 366 2 US-09-170-496D-88 Sequence 88, Appl
30 463.5 22.3 366 2 US-09-743-742B-7 Sequence 7, Appl
31 463.5 22.3 366 2 US-09-762-661A-5 Sequence 5, Appl
32 463.5 22.3 366 2 US-09-364-425B-45 Sequence 45, Appl
33 463.5 22.3 366 2 US-09-743-475-4 Sequence 4, Appl
34 462.5 22.3 366 2 US-09-170-496D-210 Sequence 210, App
35 451 21.7 349 2 US-09-762-661A-2 Sequence 2, Appl
36 437 21.1 410 2 US-08-858-876A-2 Sequence 2, Appl
37 437 21.1 410 2 US-09-472-880-2 Sequence 2, Appl
38 436 21.0 410 2 US-09-826-509-537 Sequence 537, App
39 433.5 20.9 353 1 US-08-118-270-45 Sequence 45, Appl
40 433.5 20.9 353 4 PCT-US93-08528-45 Sequence 45, Appl
41 430.5 20.7 415 2 US-09-743-742B-6 Sequence 6, Appl
42 430.5 20.7 416 2 US-08-858-876A-4 Sequence 4, Appl
43 430.5 20.7 416 2 US-09-472-880-4 Sequence 2, Appl
44 427 20.6 410 2 US-09-200-090-2 Sequence 4, Appl
45 423 20.4 302 2 US-09-077-675A-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10101
; Sequence 10101, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10101
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10101

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Best Local Similarity 79.4%; Pred. No. 6.1e-128;
Matches 312; Conservative 36; Mismatches 40; Indels 5; Gaps 1;
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Db 1 MEKLNASWIQQKLEDPFQKHLNSTEYLAFLGCPRESHPFLPSVVVYPIFVVGIGN 60
QY 56 LLVCMVIVRHQTLKTPNTYILFSLAVSDLLVLLGMPLEIYEMWNYNYPFLPGVGCYFKT 115
Db 61 VLVLVLILQHQAMKTPNTYILFSLAVSDLLVLLGMPLEIYEMWNYNYPFLPGVGCYFKT 120
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Db 121 ALFETVCFASTLSITTVTSVRYVAIVHDFRAKLRTRRALRILSLVMSFSPVPSIPNTS 180
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Db 181 IHGKIFHFPNGSLVPGSATCTVTKPMVYVNIITQATSFLLYLPMTLISLVLYLMGLRL 240
QY 236 KRDSLSLANKVAVNIHPRSRKSVTKMLFVLVLVPAICWTPPHVDRLPFPSVEEWTESLAA 295
Db 241 KKDKSLEADEGNANTIQPCRSVKNKMLFVLVLVPAICWAPPHIDRLPFPSVEEWSESLAA 300
QY 296 VFNLIHVSVGVFFYLLSSAVNPILNLLSRRFRAFRNVVSPCTCKWCHPRHRPQGPQAQKI 355